

Applicants: Bruce D. Cohen et al. Docket No.: ABX-PF2 US  
 Application No.: To Be Assigned Filed: Herewith  
 For: ANTIBODIES TO INSULIN-LIKE GROWTH Express Mail No.  
 Factor I Receptor  
 Agent: Karen E. Brown, Reg. No. 43,866 Sheet 1 of 25 EL 889410403 US

2.13.2K	GACATCCAGA	TGACCCAGTT	TCCATCCTCC	CTGTCTGCAT	CTGTAGGAGA	50
A30	GACATCCAGA	TGACCCAGTC	TCCATCCTCC	CTGTCTGCAT	CTGTAGGAGA	50
2.14.3K	-----	-----	-TCCCT	CTGTCTGCAT	CTGTAGGAGA	26
2.12.1K	-----	-----	-----	TGCAT	CTGTAGGAGA	15
4.9.2K	GACATCCAGA	TGACCCAGTC	TCCATCCTCC	CTGTCTGCAT	CTGTAGGAGA	50
Consensus	GACATCCAGA	TGACCCAGTT	TCCATCCTCC	CTGTCTGCAT	CTGTAGGAGA	50
				CDR1		
2.13.2K	CAGAGTCACC	ATCACTTGGC	GGGCAAGTCA	GGCATTAGA	AATGATTTAG	100
A30	CAGAGTCACC	ATCACTTGGC	GGGCAAGTCA	GGCATTAGA	AATGATTTAG	100
2.14.3K	CAGAGTCACC	TTCACTTGGC	GGGCAAGTCA	GGCATTAGA	CGTGATTTAG	76
2.12.1K	CAGAGTCACC	TTCACTTGGC	GGGCAAGTCA	GGCATTAGA	CGTGATTTAG	65
4.9.2K	CAGAGTCACC	ATCACTTGGC	GGGCAAGTCA	GGCATTAGA	AATGATTTAG	100
Consensus	CAGAGTCACC	WTCACTTGGC	GGGCAAGTCA	GGCATTAGA	MRTGATTTAG	100
				CDR2		
2.13.2K	GCTGGTATCA	GCAGAAAACCA	GGGAAAGGCC	CTAACGGCCT	GATCTATGCT	150
A30	GCTGGTATCA	GCAGAAAACCA	GGGAAAGGCC	CTAACGGCCT	GATCTATGCT	150
2.14.3K	GCTGGTATCA	GCAGAAAACCA	GGGAAAGGCC	CTAACGGCCT	GATCTATGCT	126
2.12.1K	GCTGGTATCA	GCAGAAAACCA	GGGAAAGGCC	CTAACGGCCT	GATCTATGCT	115
4.9.2K	GCTGGTATCA	GCAGAAAACCA	GGGAAAGGCC	CTAACGGCCT	GATCTATGCT	150
Consensus	GCTGGTATCA	GCAGAAAACCA	GGGAAAGGCC	CTAACGGCCT	GATCTATGCT	150
				CDR3		
2.13.2K	GCATCCCGTT	TSCACAGGG	GGTCCCCATCA	AGGTTCAGCG	GCAGTGGATC	200
A30	GCATCCCGTT	TSCACAGGG	GGTCCCCATCA	AGGTTCAGCG	GCAGTGGATC	200
2.14.3K	GCATCCCGTT	TACAAAGGG	GGTCCCCATCA	AGGTTCAGCG	GCAGTGGATC	176
2.12.1K	GCATCCCGTT	TACAAAGGG	GGTCCCCATCA	AGGTTCAGCG	GCAGTGGATC	165
4.9.2K	GCATCCCGTT	TACACGGGG	GGTCCCCATCA	AGGTTCAGCG	GCAGTGGATC	200
Consensus	GCATCCCGTT	TSCACAGGG	GGTCCCCATCA	AGGTTCAGCG	GCAGTGGATC	200
				CDR3		
2.13.2K	TGGGACAGAA	TTCACTCTCA	CAATCAGCG	CCTGCAGCCT	GAAGATTTTG	250
A30	TGGGACAGAA	TTCACTCTCA	CAATCAGCG	CCTGCAGCCT	GAAGATTTTG	250
2.14.3K	TGGGACAGAA	TTCACTCTCA	CAATCAGCG	CCTGCAGCCT	GAAGATTTTG	226
2.12.1K	TGGGACAGAA	TTCACTCTCA	CAATCAGCG	CCTGCAGCCT	GAAGATTTTG	215
4.9.2K	TGGGACAGAA	TTCACTCTCA	CAATCAGCG	CCTGCAGCCT	GAAGATTTTG	250
Consensus	TGGGACAGAA	TTCACTCTCA	CAATCAGCG	CCTGCAGCCT	GAAGATTTTG	250
				CDR3		
2.13.2K	CAACTTATTA	CTGTCTACAA	CATAATACTT	ACCCGTGCG	TTTGGCCAG	300
A30	CAACTTATTA	CTGTCTACAG	CATAATACTT	ACCC-TCCN-	-----	288
2.14.3K	CAACTTATTA	CTGTCTACAG	CATAATACTT	ACCCCTGGAC	GTTCGGCCAA	276
2.12.1K	CAACTTATTA	CTGTCTACAG	CATAATACTT	ACCCCTGGAC	GTTCGGCCAA	265
4.9.2K	CAACTTATTA	CTGTCTACAG	CATAATACTT	ACCCCTCTAC	TTTCGGCGGA	300
Consensus	CAACTTATTA	CTGTCTACAG	CATAATACTT	ACCCKYBSNS	KTTYGGCSRR	300
2.13.2K	GGGACCAAGC	TGGAGATCAA	AC----			322
A30	-----	-----	-----			288
2.14.3K	GGGACCGAGG	TGGAATCAT	ACGAAC			302
2.12.1K	GGGACCGAGG	TGGAATCAT	ACGAAC			291
4.9.2K	GGGACCAAGG	TGGAGATCAA	AC----			322
Consensus	GGGACCRAGS	TGGARATCAW	ACGAAC			326

FIG. 1A

4.17.3K	-----	-----	-----	AGGAGA	7
O12	GACATCCAGA	TGACCCAGTC	TCCATCCCTCC	CTGTCTGCAT	CTGTAAGGAGA
Consensus	GACATCCAGA	TGACCCAGTC	TCCATCCCTCC	CTGTCTGCAT	CTGYAGGAGA
CDR1					
4.17.3K	CAGAGTCACC	ATCACTTGGC	GGGCAAGTCA	GAGCATTAGT	ACCTTTAA
O12	CAGAGTCACC	ATCACTTGGC	GGGCAAGTCA	GAGCATTAGT	ACCTTTAA
Consensus	CAGAGTCACC	ATCACTTGGC	GGGCAAGTCA	GAGCATTAGT	ACCTTTAA
CDR2					
4.17.3K	ATGGGTATCA	GCAGAAAACCA	GGGAAAGCCC	CTAACTCTCT	GATCATGTT
O12	ATGGGTATCA	GCAGAAAACCA	GGGAAAGCCC	CTAACTCTCT	GATCATGTT
Consensus	ATGGGTATCA	GCAGAAAACCA	GGGAAAGCCC	CTAACTCTCT	GATCATGTT
CDR2					
4.17.3K	GCATCCAGTT	TTCAACTTGG	GGTCCCCATCA	AGGTTCACTG	GCAGTGGATC
O12	GCATCCAGTT	TTCAACTTGG	GGTCCCCATCA	AGGTTCACTG	GCAGTGGATC
Consensus	GCATCCAGTT	TTCAACTTGG	GGTCCCCATCA	AGGTTCACTG	GCAGTGGATC
CDR3					
4.17.3K	TGGGACAGAT	TTCACTCTCA	CCATCAGCAG	TCTGCAACCT	GAAGATTTTG
O12	TGGGACAGAT	TTCACTCTCA	CCATCAGCAG	TCTGCAACCT	GAAGATTTTG
Consensus	TGGGACAGAT	TTCACTCTCA	CCATCAGCAG	TCTGCAACCT	GAAGATTTTG
CDR3					
4.17.3K	CAACTTACTA	CTGTCAACAG	AGTTACATTC	CCCCACTCAC	TTTCGGCGGA
O12	CAACTTACTA	CTGTCAACAG	AGTTACATTC	CCCC-TCC-	-----
Consensus	CAACTTACTA	CTGTCAACAG	AGTTACATTC	CCCCAYYHC	TTTCGGCGGA
4.17.3K	GGGACCAAGG	TGGAGATCAA	AC	-----	279
O12	-----	-----	-----	-----	288
Consensus	GGGACCAAGG	TGGAGATCAA	AC	-----	322

FIG. 1B

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Agent: Karen E. Brown, Reg. No. 43,866 Sheet 3 of 25

6.1.1K	GAAATTGTGT	TGACGCAGTC	TCCAGGCC	CTGCTTTGT	CTCCAGGGGA	50
A27	GAAATTGTGT	TGACGCAGTC	TCCAGGCC	CTGCTTTGT	CTCCAGGGGA	50
Consensus	GAAATTGTGT	TGACGCAGTC	TCCAGGCC	CTGCTTTGT	CTCCAGGGGA	50
			CDR1			
6.1.1K	AGAGGCCACC	CTCTCCTCGA	GGGCCAGTCA	GAGTGTGTC	GGCAGCTACT	49
A27	AGAGGCCACC	CTCTCCTCGA	GGGCCAGTCA	GAGTGTGTC	GGCAGCTACT	100
Consensus	AGAGGCCACC	CTCTCCTCGA	GGGCCAGTCA	GAGTGTGTC	GGCAGCTACT	100
6.1.1K	TAGCCCTGGTA	CCAGCAGAAA	CCTGGCCAGG	CTCCCAGGCT	CCTCATCTAT	99
A27	TAGCCCTGGTA	CCAGCAGAAA	CCTGGCCAGG	CTCCCAGGCT	CCTCATCTAT	150
Consensus	TAGCCCTGGTA	CCAGCAGAAA	CCTGGCCAGG	CTCCCAGGCT	CCTCATCTAT	150
	CDR2					
6.1.1K	GGTGCATCCA	GCAGGGCCAC	TGGCATCCCA	GACAGGTTCA	GTGGCAGTGG	149
A27	GGTGCATCCA	GCAGGGCCAC	TGGCATCCCA	GACAGGTTCA	GTGGCAGTGG	200
Consensus	GGTGCATCCA	GCAGGGCCAC	TGGCATCCCA	GACAGGTTCA	GTGGCAGTGG	200
6.1.1K	GTCTGGGACA	GACTTCACTC	TCACCATCAT	CAGACTGGAG	CCTGAAGATT	199
A27	GTCTGGGACA	GACTTCACTC	TCACCATCAT	CAGACTGGAG	CCTGAAGATT	250
Consensus	GTCTGGGACA	GACTTCACTC	TCACCATCAT	CAGACTGGAG	CCTGAAGATT	250
	CDR3					
6.1.1K	TTGCACTGTT	TTACTCTTCAG	CAGTATGGTA	CTTCACCTCG	NACGTTCCGC	249
A27	TTGCACTGTT	TTACTCTTCAG	CAGTATGGTA	CTTCACCTCG	NACGTTCCGC	290
Consensus	TTGCACTGTT	TTACTCTTCAG	CAGTATGGTA	CTTCACCTCG	NACGTTCCGC	300
6.1.1K	CAAGGGACCA	AGGTGGAAT	CAAAC			274
A27	-----	-----	CAAAC			290
Consensus	CAAGGGACCA	AGGTGGAAT	CAAAC			325

**FIG. 1C**

2.12.1H	-----	-----	GGGAGGC TTGGTCAAGC CTGGAGTC	26
DP35	CAGGTGCAGC	TGGTGGAGTC	TGGGGGAGGC TTGGTCAAGC CTGGAGGGTC	50
Consensus	CAGGTGCAGC	TGGTGGAGTC	TGGGGGAGGC TTGGTCAAGC CTGGAGGGTC	50
			CDR1	
2.12.1H	CCTGAGACTC	TCCCTGTGCAG	CCTCTGGATT CACCTTCAGT GACTACTAC	76
DP35	CCTGAGACTC	TCCCTGTGCAG	CCTCTGGATT CACCTTCAGT GACTACTAC	100
Consensus	CCTGAGACTC	TCCCTGTGCAG	CCTCTGGATT CACCTTCAGT GACTACTAC	100
			CDR2	
2.12.1H	TGAGCTGGAT	CCGCCAGGCT	CCAGGGAAAGG GGCTGGATG GGTTTCATAC	126
DP35	TGAGCTGGAT	CCGCCAGGCT	CCAGGGAAAGG GGCTGGATG GGTTTCATAC	150
Consensus	TGAGCTGGAT	CCGCCAGGCT	CCAGGGAAAGG GGCTGGATG GGTTTCATAC	150
			CDR2	
2.12.1H	ATTAGTAGTA	GTGGTAGTAC	CACACTACTAC GCAGACTCTG TGAAAGGGCCG	176
DP35	ATTAGTAGTA	GTGGTAGTAC	CACACTACTAC GCAGACTCTG TGAAAGGGCCG	200
Consensus	ATTAGTAGTA	GTGGTAGTAC	CACACTACTAC GCAGACTCTG TGAAAGGGCCG	200
			CDR3	
2.12.1H	ATTCACCATC	TCCAGGGACA	ACGCCAAGAA CTCACTGTAT CTGCAAATGA	226
DP35	ATTCACCATC	TCCAGGGACA	ACGCCAAGAA CTCACTGTAT CTGCAAATGA	250
Consensus	ATTCACCATC	TCCAGGGACA	ACGCCAAGAA CTCACTGTAT CTGCAAATGA	250
			CDR3	
2.12.1H	ACAGCCTGAG	AGCCGAGGAC	ACGGCCGTGT ATTACTGTGT GAGAGATGGA	276
DP35	ACAGCCTGAG	AGCCGAGGAC	ACGGCCGTGT ATTACTGTGT GAGAGA---	296
Consensus	ACAGCCTGAG	AGCCGAGGAC	ACGGCCGTGT ATTACTGTGT GAGAGATGGA	300
			CDR3	
2.12.1H	GTTGGAAACTA	CTTTTTACTA	CTACTACTAC GGTATGGACG TCTGGGGCCA	326
DP35	-----	-----	-----	296
Consensus	GTTGGAAACTA	CTTTTTACTA	CTACTACTAC GGTATGGACG TCTGGGGCCA	350
			CDR3	
2.12.1H	AGGGACCACG	GTCACCGTCT	CCTCAG	352
DP35	-----	-----	-----	296
Consensus	AGGGACCACG	GTCACCGTCT	CCTCAG	376

FIG. 2A

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PF2-2.14.3H.DNA	-----	GGGCCCCAGGA	CTGGTGAAGC	CTTCGGAGAC	
VIV-4/4.35	CAGGTGCAGC	TGCAGGAGTC	GGGCCCAAGGA	CTGGTGAAGC	CTTCGGAGAC
Consensus	CAGGTGCAGC	TGCAGGAGTC	GGGCCCAAGGA	CTGGTGAAGC	CTTCGGAGAC
					30
					50
					50
PF2-2.14.3H.DNA	-----	GGGCCCCAGGA	CTGGTGAAGC	CTTCGGAGAC	
VIV-4/4.35	CCTGTCCTC	ACCTGCACTG	TCTCTGGTGG	CTCCATCAGT	AATTACTACT
Consensus	CCTGTCCTC	ACCTGCACTG	TCTCTGGTGG	CTCCATCAGT	AATTACTACT
					80
					100
					100
PF2-2.14.3H.DNA	-----	GGGCCCCAGGA	CTGGTGAAGC	CTTCGGAGAC	
VIV-4/4.35	GGAGCTGGAT	CGGGCAGCCC	GCCGGAAAGG	GACTGGAGTG	GATTGGGGGT
Consensus	GGAGCTGGAT	CGGGCAGCCC	GCCGGAAAGG	GACTGGAGTG	GATTGGGGGT
					130
					150
					150
PF2-2.14.3H.DNA	-----	GGGCCCCAGGA	CTGGTGAAGC	CTTCGGAGAC	
VIV-4/4.35	ATCTATACCA	GTGGGAGC	CCAACTAACAC	CCCTCCCTCA	AGAGTCGAGT
Consensus	ATCTATACCA	GTGGGAGC	CCAACTAACAC	CCCTCCCTCA	AGAGTCGAGT
					180
					200
					200
PF2-2.14.3H.DNA	-----	GGGCCCCAGGA	CTGGTGAAGC	CTTCGGAGAC	
VIV-4/4.35	CACCATGTCA	GTAGACACGT	CCAAGAACCA	GTTCTCCCTG	AAAGCTGACT
Consensus	CACCATGTCA	GTAGACACGT	CCAAGAACCA	GTTCTCCCTG	AAAGCTGACT
					230
					250
					250
PF2-2.14.3H.DNA	-----	GGGCCCCAGGA	CTGGTGAAGC	CTTCGGAGAC	
VIV-4/4.35	CTGTGACCGC	CGCGGACACG	GCCGTGTATT	ACTGTGCG	AACGATTTTT
Consensus	CTGTGACCGC	CGCGGACACG	GCCGTGTATT	ACTGTGCG	AACGATTTTT
					280
					288
					300
PF2-2.14.3H.DNA	-----	GGGCCCCAGGA	CTGGTGAAGC	CTTCGGAGAC	
VIV-4/4.35	GGAGTGGTTA	TTATCTTTGA	CTACTGGGGC	CACCGAACCC	TGGTCACCGT
Consensus	GGAGTGGTTA	TTATCTTTGA	CTACTGGGGC	CACCGAACCC	TGGTCACCGT
					330
					340
					350
PF2-2.14.3H.DNA	-----	GGGCCCCAGGA	CTGGTGAAGC	CTTCGGAGAC	
VIV-4/4.35	CTCCTCA	-----	-----	-----	-----
Consensus	CTCCTCA	-----	-----	-----	-----
					338
					344
					358

FIG. 2B

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6.1.1H	GAGGTGCAGC	TGTTGGAGTC	TGGGGGAGGC	TTGGTACAGC	CTGGGGGGTC	50
4.9.2H	GAGGTGCAGC	TGTTGGAGTC	TGGGGGAGGC	TTGGTACAGC	CTGGGGGGTC	50
DP47	GAGGTGCAGC	TGTTGGAGTC	TGGGGGAGGC	TTGGTACAGC	CTGGGGGGTC	50
2.13.2H	GAGGTGCAGC	TGTTGGAGTC	TGGGGGAGGC	TTGGTACAGC	CTGGGGGGTC	50
Consensus	GAGGTGCAGC	TGTTGGAGTC	TGGGGGAGGC	TTGGTACAGC	CTGGGGGGTC	50
				CDR1		
6.1.1H	CCTGAGACTC	TCCTGTCAAG	CCTCTGGATT	CACCTTTAGC	AGCTATGCCA	100
4.9.2H	CCTGAGACTC	TCCTGTCAAG	CCTCTGGATT	CACCTTTAGC	AGCTATGCCA	100
DP47	CCTGAGACTC	TCCTGTCAAG	CCTCTGGATT	CACCTTTAGC	AGCTATGCCA	100
2.13.2H	CCTGAGACTC	TCCTGTCAAG	CCTCTGGATT	CACCTTTAGC	AGCTATGCCA	100
Consensus	CCTGAGACTC	TCCTGTCAAG	CCTCTGGATT	CACCTTTAGC	AGCTATGCCA	100
				CDR1	CDR2	
6.1.1H	TGACTCTGGGT	CGGCCAGGCT	CCAGGGAAAG	GGCTGGAGTG	GGTCTCACGTT	150
4.9.2H	TGACTCTGGGT	CGGCCAGGCT	CCAGGGAAAG	GGCTGGAGTG	GGTCTCACGTT	150
DP47	TGACTCTGGGT	CGGCCAGGCT	CCAGGGAAAG	GGCTGGAGTG	GGTCTCACGTT	150
2.13.2H	TGACTCTGGGT	CGGCCAGGCT	CCAGGGAAAG	GGCTGGAGTG	GGTCTCACGTT	150
Consensus	TGACTCTGGGT	CGGCCAGGCT	CCAGGGAAAG	GGCTGGAGTG	GGTCTCACGTT	150
				CDR2		
6.1.1H	ATTAGCTGGTA	GTGGTGGTAG	TACATTCCTAC	GCAGACTCCG	TGAAGGGCCG	200
4.9.2H	ATTAGCTGGTA	GTGGTGGTAG	CACATTCCTAC	GCAGACTCCG	TGAAGGGCCG	200
DP47	ATTAGCTGGTA	GTGGTGGTAG	CACATTCCTAC	GCAGACTCCG	TGAAGGGCCG	200
2.13.2H	ATTAGCTGGTA	GTGGTGGTAG	CACATTCCTAC	GCAGACTCCG	TGAAGGGCCG	200
Consensus	ATTAGCTGGTA	GTGGTGGTAG	YACATTCCTAC	GCAGACTCCG	TGAAGGGCCG	200
6.1.1H	GTTCACCACATC	TCCAGAGACA	ATTCCAGAGACA	CACGCTGTAT	CTGCAAATGA	250
4.9.2H	GTTCACCACATC	TCCAGAGACA	ATTCCAGAGACA	CACGCTGTAT	CTGCAAATGA	250
DP47	GTTCACCACATC	TCCAGAGACA	ATTCCAGAGACA	CACGCTGTAT	CTGCAAATGA	250
2.13.2H	GTTCACCACATC	TCCAGAGACA	ATTCCAGAGACA	CACGCTGTAT	CTGCAAATGA	250
Consensus	GTTCACCACATC	TCCAGAGACA	ATTCCAGAGACA	CACGCTGTAT	CTGCAAATGA	250
				CDR3		
6.1.1H	ACAGCCTGAG	ACCGCAGGAC	ACGGCCGTAT	ATTACTGTGC	GAAGATC--	298
4.9.2H	ACAGCCTGAG	ACCGCAGGAC	ACGGCCGTAT	ATTACTGTGC	GAAGATCTG	300
DP47	ACAGCCTGAG	ACCGCAGGAC	ACGGCCGTAT	ATTACTGTGC	GAAGA---	296
2.13.2H	ACAGCCTGAG	ACCGCAGGAC	ACGGCCGTAT	ATTACTGTGC	GAAGATCTT	300
Consensus	ACAGCCTGAG	ACCGCAGGAC	ACGGCCGTAT	ATTACTGTGC	GAAGATCTK	300
				CDR3-for 4.9.2 and 2.13.2		
6.1.1H	-----	-----	-----	-----	-C-	299
4.9.2H	GGCTACGGTG	ACTTTTACTA	CTACTACTAC	GGTATGGACG	TCTGGGGCCA	350
DP47	-----	-----	-----	-----	-----	296
2.13.2H	GGCTGGTCG	ACTCTTACTA	CTACTACTAC	GGTATGGACG	TCTGGGGCCA	350
Consensus	GGCTRSKSYG	ACTYTTACTA	CTACTACTAC	GGTATGGACG	TCTGGGGCCA	350
				CDR3-for 6.1.1		
6.1.1H	AGGGACTACG	GTGATTATGA	GTGGTTCGA	CCCCCTGGGGC	CAGGGAAACCC	349
4.9.2H	AGGGACCA-	-----	-----	-----	-----	359
DP47	-----	-----	-----	-----	-----	296
2.13.2H	AGGGACCA-	-----	-----	-----	-----	359
Consensus	AGGGACYACG	GTGATTATGA	GTGGTTCGA	CCCCCTGGGGC	CAGGGAAACCC	400

FIG. 2C-1

6.1.1H	TGGTCACCGT	CTCCTCAG	367
4.9.2H	-GGTCACCGT	CTCCTCAG	376
DP47	-----	-----	296
2.13.2H	-GGTCACCGT	CTCCTCAG	376
Consensus	TGGTCACCGT	CTCCTCAG	418

## FIG. 2C-2

4.17.3H	-----	-----	CCCAGGA	CTGGTGAAAGC	CTTCGGAGAC	27
DP71	CAGGTGCAGC	TGCAAGGAGTC	GGGCCAGGA	CTGGTGAAAGC	CTTCGGAGAC	50
Consensus	CAGGTGCAGC	TGCAAGGAGTC	GGCCCAGGA	CTGGTGAAAGC	CTTCGGAGAC	50
					CDR1	
4.17.3H	CCTGTCCCTC	ACCTGCACTG	TCTCTGGTGG	CTCCATCACTG	AGTTACTACT	77
DP71	CCTGTCCCTC	ACCTGCACTG	TCTCTGGTGG	CTCCATCACTG	AGTTACTACT	100
Consensus	CCTGTCCCTC	ACCTGCACTG	TCTCTGGTGG	CTCCATCACTG	AGTTACTACT	100
		CDR1				
4.17.3H	GGAGCTGGAT	CCGGCAGCCC	CCAGGGAAAGG	GACTGGAGTG	GATTGGTAT	127
DP71	GGAGCTGGAT	CCGGCAGCCC	CCAGGGAAAGG	GACTGGAGTG	GATTGGTAT	150
Consensus	GGAGCTGGAT	CCGGCAGCCC	CCAGGGAAAGG	GACTGGAGTG	GATTGGTAT	150
		CDR2				
4.17.3H	ATCTATTACA	GTGGGAGCAC	CAAATCACAC	CCCTCCCTCA	AGAGTCGAGT	177
DP71	ATCTATTACA	GTGGGAGCAC	CAAATCACAC	CCCTCCCTCA	AGAGTCGAGT	200
Consensus	ATCTATTACA	GTGGGAGCAC	CAAATCACAC	CCCTCCCTCA	AGAGTCGAGT	200
4.17.3H	CACCATATCA	GTAGACACGT	CCAAGAACCA	GTTCTCCCTG	AAGCTGAGCT	227
DP71	CACCATATCA	GTAGACACGT	CCAAGAACCA	GTTCTCCCTG	AAGCTGAGCT	250
Consensus	CACCATATCA	GTAGACACGT	CCAAGAACCA	GTTCTCCCTG	AAGCTGAGCT	250
		CDR3				
4.17.3H	CTGTGACCGC	TGGGGACACG	GCCGTGTATT	ACTGTGCGAG	GACGTATAGC	277
DP71	CTGTGACCGC	TGGGGACACG	GCCGTGTATT	ACTGTGCGAG	GA-----	289
Consensus	CTGTGACCGC	TGGGGACACG	GCCGTGTATT	ACTGTGCGAG	GACGTATAGC	300
4.17.3H	AGTCGTTCT	ACTACTACGG	TATGGACGTC	TGGGGCCAAG	GGACCACGGT	327
DP71	-----	-----	GA-----	GA-----	GA-----	293
Consensus	AGTCGTTCT	ACTACTACGG	TATGGACGTC	TGGGGCCAAG	GGACCACGGT	350
4.17.3H	CACCGTCTCC	TCAG				341
DP71	-----	-----				293
Consensus	CACCGTCTCC	TCAG				364

## FIG. 2D

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To Be Assigned  
ANTIBODIES TO INSULIN-LIKE GROWTH  
FACTOR I RECEPTOR  
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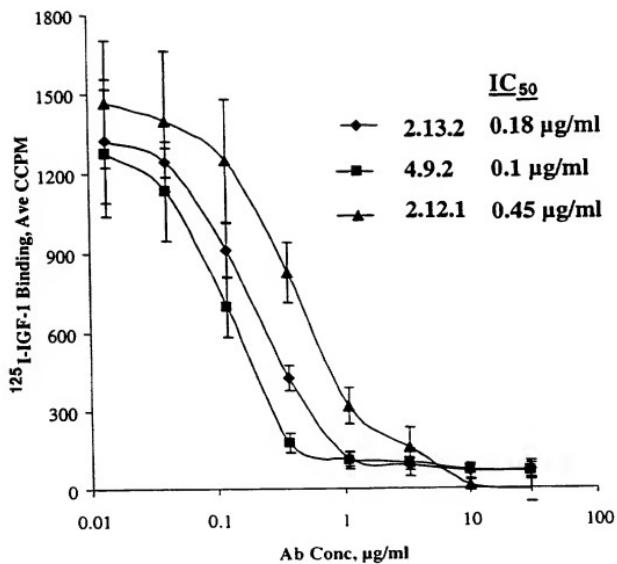


FIG. 3

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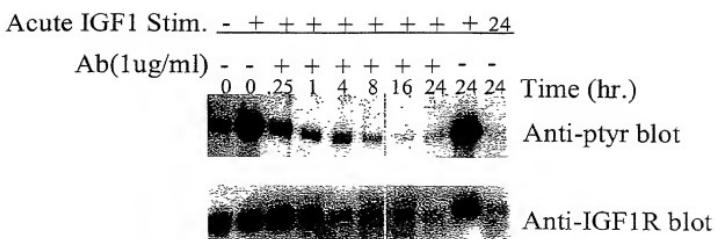


FIG. 4

Applicants:  
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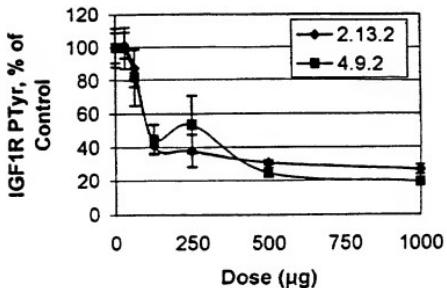


FIG. 5

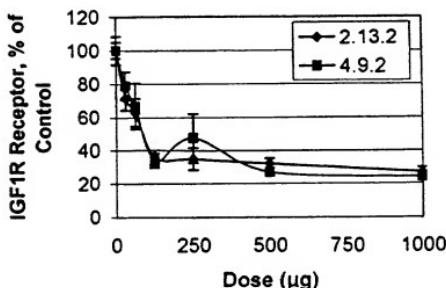


FIG. 6

Combination with Adriamycin

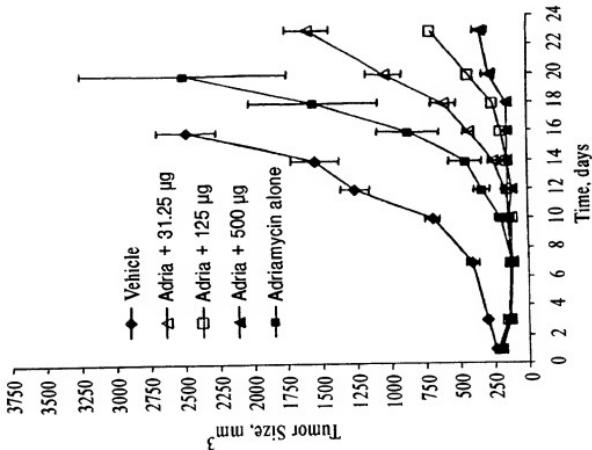
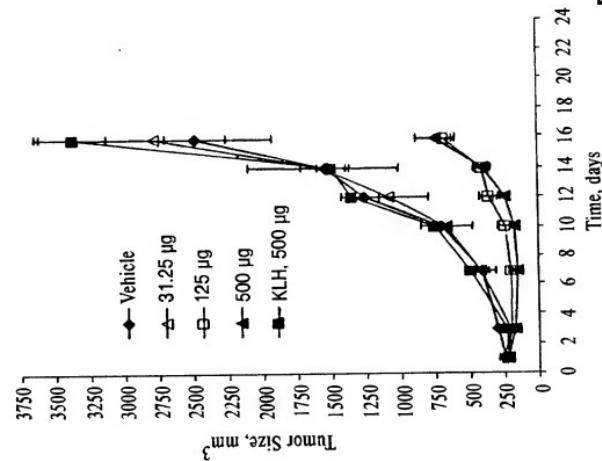


FIG. 7

Treatment: 125 µg dose

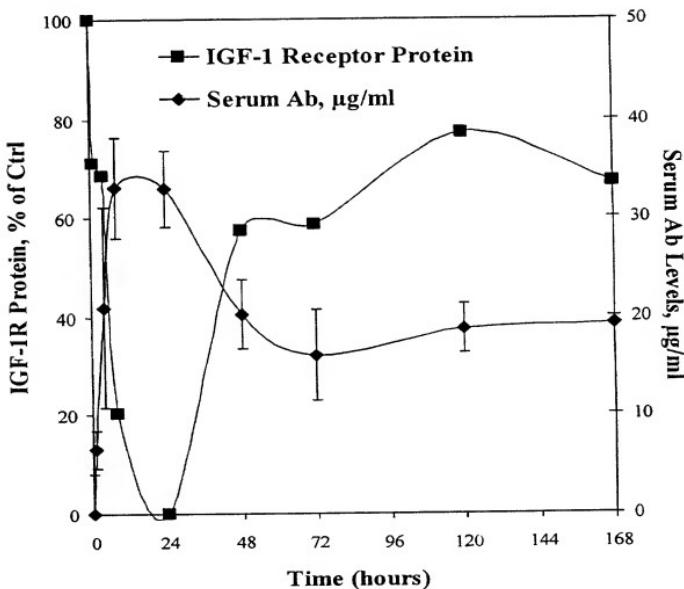


FIG. 8

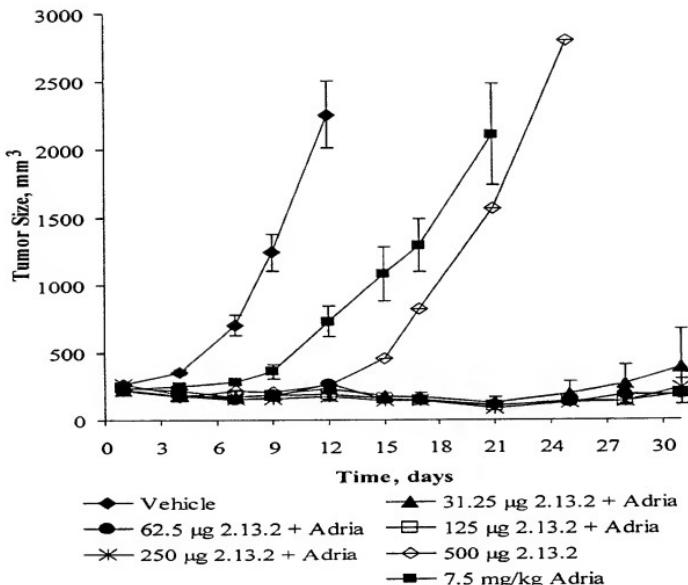


FIG. 9

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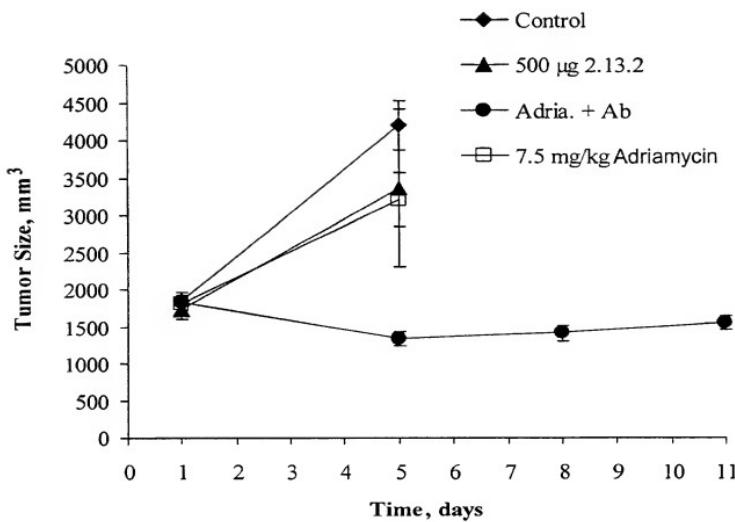


FIG. 10

Combination

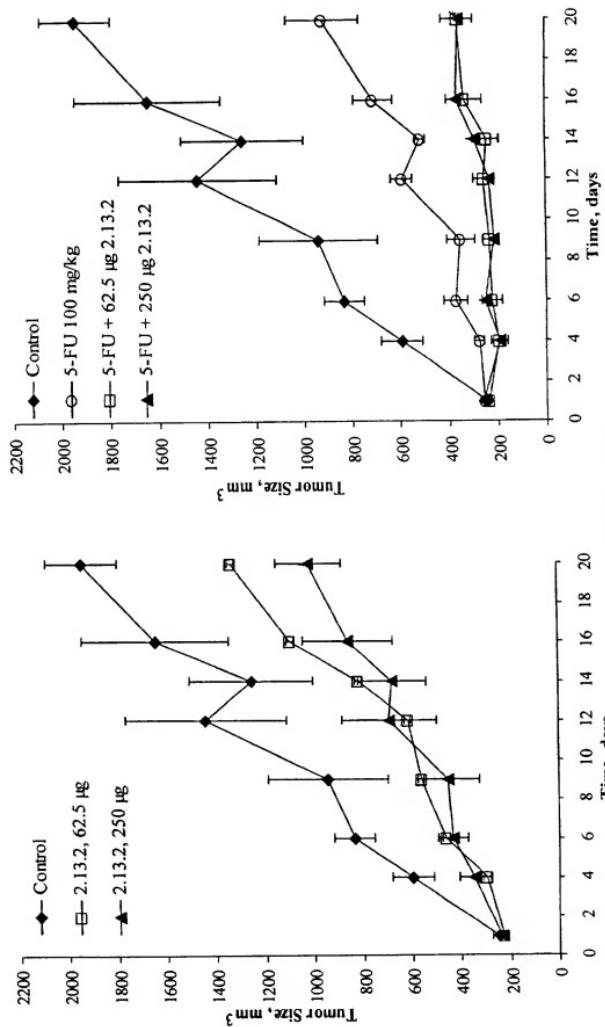


FIG. 11

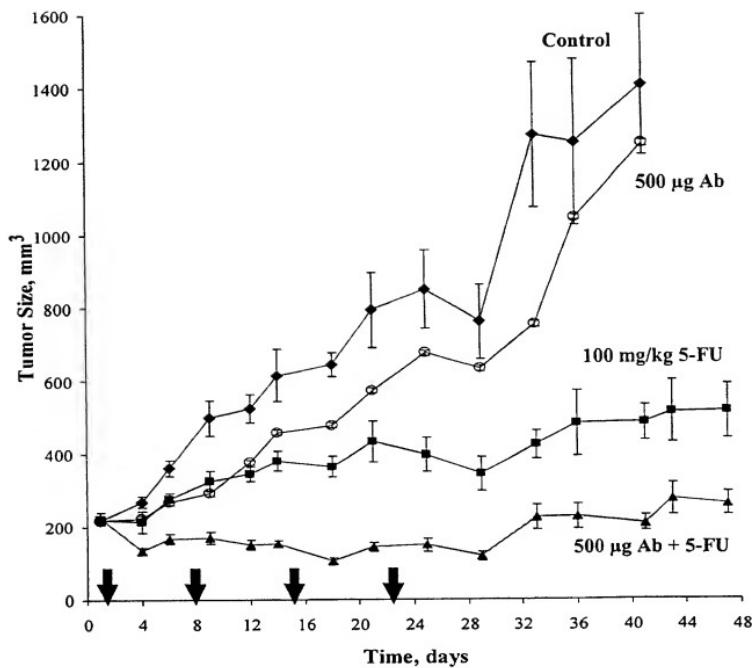


FIG. 12

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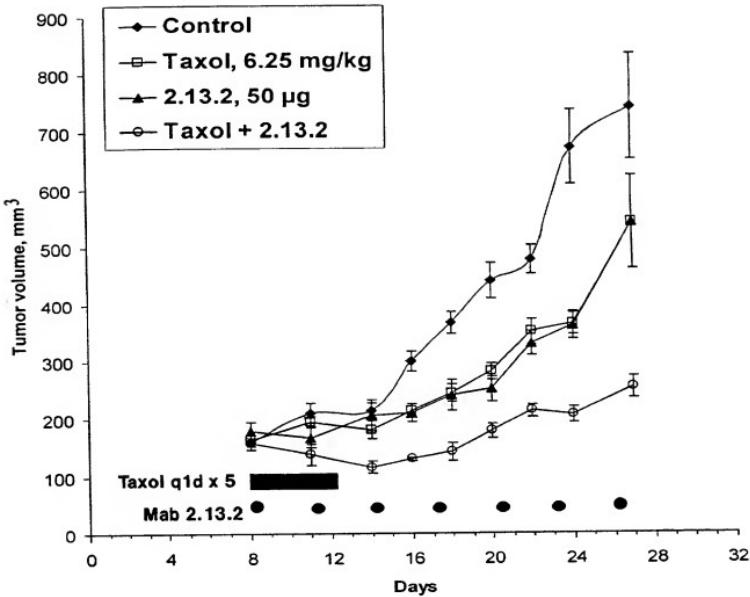


FIG. 13

## Single Agent Combination

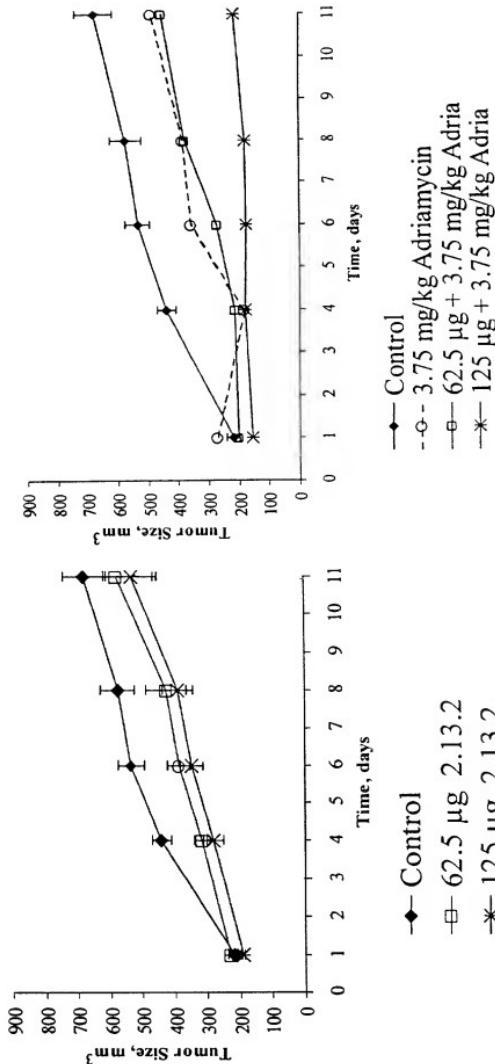


FIG. 14

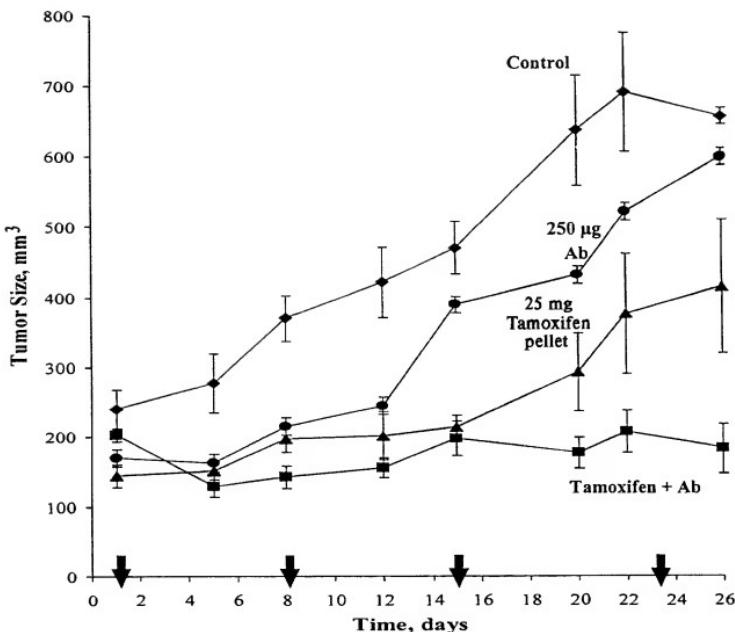


FIG. 15

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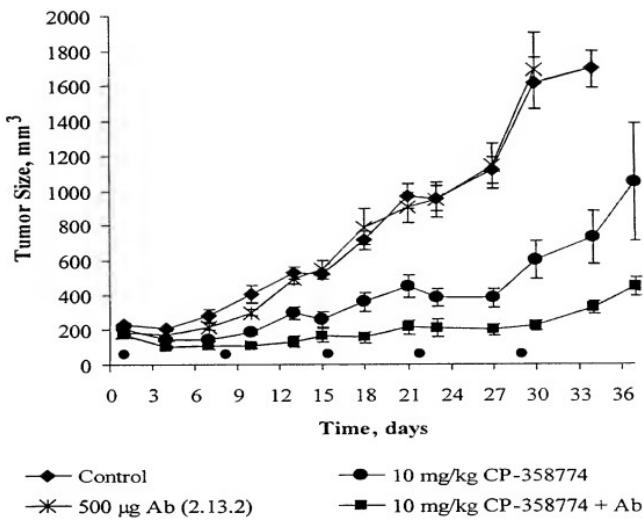


FIG. 16

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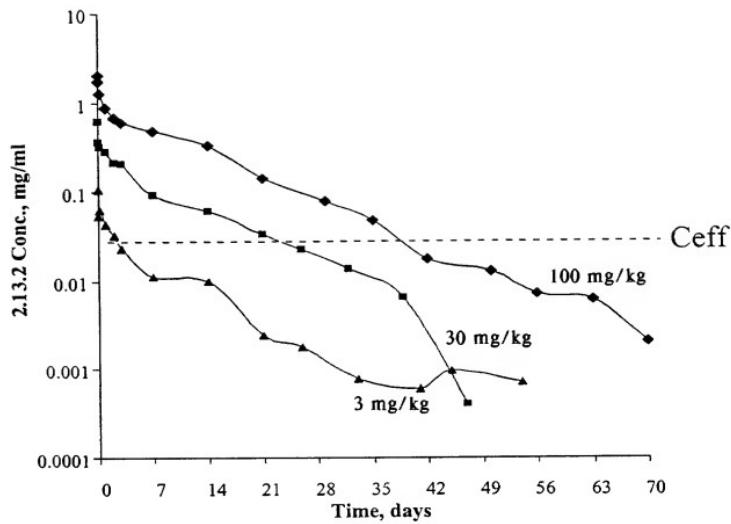


FIG. 17

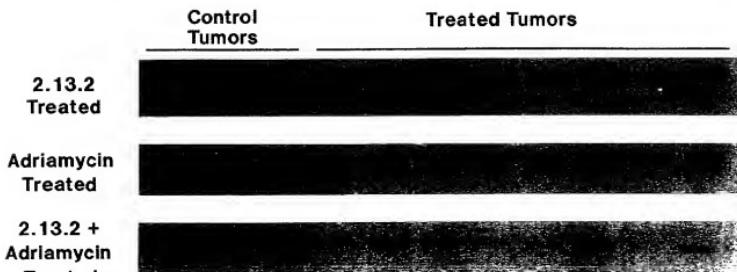


FIG. 18

Clone	C domain mutations	FR mutation	CDR mutation	Change in Cys	Change in glycosylation
2.13.2 Heavy	0	3	8	0	0
2.13.2 Light	0	1	4	1 (CDR3)	0
2.12.2 Heavy	0	2	8	0	0
2.12.2 Light	0	3	5	0	0

FIG. 19A

FIG. 19B

PF2 2.13.2 LC (A30/JK2) \*

MDMVPAQLL GLILLWPPGA RCDIQTOPP SSSLASVGRD VTIICRASQG IRNDLGYQQ KFGKAPKRRI YAASPLHGV PSFPGSGSG TETLTISSSL  
MDMVPAQLL GLILLWPPGA RCDIQTOPP SSSLASVGRD VTIICRASQG IRNDLGYQQ KFGKAPKRRI YAASPLHGV PSFPGSGSG TETLTISSSL

\*\*\* QPEDPATYC LQHNSYPCST GQGTLEIKER TVAAPSVIF PPSEBQLKSG TAVUCLLAN FYPREAKYQW KVDNALQSGN SQESVTQDS KDTSYLSLST  
QPEDPATYC LQHNSYPCST GQGTLEIKER TVAAPSVIF PPSEBQLKSG TAVUCLLAN FYPREAKYQW KVDNALQSGN SQESVTQDS KDTSYLSLST

LTLSDADYEK HKTYACEVTH QGLISSPVTKS FNRGEC  
LTLSDADYEK HKTYACEVTH QGLISSPVTKS FNRGEC

### FIG. 19C

PF2 2.12.1 Heavy chain (DP-35(3-11)/D1-3/JH6)

\* \* \* \* \* NEFGLSWVPL VALIKGPQQC AQLVBSGGGL VKPGGSLRLS CAASGFTYSD YTMWSIRQAP GKGLIHWVSYI SSSGGKRTTIS RDNAKNSLYL  
NEFGLSWVPL VALIKGPQQC AQLVBSGGGL VKPGGSLRLS CAASGFTYSD YTMWSIRQAP GKGLIHWVSYI SSSGGKRTTIS RDNAKNSLYL

\*\*\* QNSIRADT AVYCYR-D GVECTP-XXX YYGMDVWQGQ TTIVVSSAST KGFSVPLAP CSRSTSESTA ALGCLVQDYF PEPVTSWNS GALTSVHTF  
QNSIRADT AVYCYARVL FLMLLTTYY YIGGDWQGQ TTIVVSSAST KGFSVPLAP CSRSTSESTA ALGCLVQDYF PEPVTSWNS GALTSVHTF

PAVLOSSLY SLSVVTVPS SNGQTQTVTC NVDHKPSTK VDKTVERKCC VECPPCPAPP VAGPSVFLPP PKPKDTLMIS RPEVTCVVV DVSHEDBEVQ  
PAVLOSSLY SLSVVTVPS SNGQTQTVTC NVDHKPSTK VDKTVERKCC VECPPCPAPP VAGPSVFLPP PKPKDTLMIS RPEVTCVVV DVSHEDBEVQ

FNWYDGVEV HNAKTRPREE QNSTFRVVS VLTIVHQDWL NGREYKEKVS NKGLPAPIEK TISKTKGQPRE PoyTlLPPS REEMTKQVS LTLCLVKGFP  
FNWYDGVEV HNAKTRPREE QNSTFRVVS VLTIVHQDWL NGREYKEKVS NKGLPAPIEK TISKTKGQPRE PoyTlLPPS REEMTKQVS LTLCLVKGFP

SDIAVEMESN GOPENNYKTT PPMLDSDGSF FLYSKLTVDK SRM0QGNVFS CSVMEHALIN HYTQSLSLSP GK  
SDIAVEMESN GOPENNYKTT PPMLDSDGSF FLYSKLTVDK SRM0QGNVFS CSVMEHALIN HYTQSLSLSP GK

### FIG. 19D

Applicants:  
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PP2.12.1 Light chain (A30/JK1) \* \* \* \* \*

MDDMRYPAQQL GLLLNTPGA RCDIQMTQSP SSSLASVQDR VTFPCRASQD IRDLGMYQQ KPGKAPKRLL YAAISLQSGV PSRFSGSQG TEFTLTISSL  
MDMRYPQQL GLLLNTPGA RCTIQMTQSP SSSLASVQDR VTCRASQD IRDLGMYQQ KEGKAPKRLL YAAISLQSGV PSRFSGSQG TEFTLTISSL  
QPEDFATYC LQHNTYPTTF GOTTEYELL TVAAPSVFLF PPSEDEQLKSG TASVCLNN FYPREAKVW KVDNALQSGN SOESVTBODS KOSTYSLST  
QPEDFATYC LQHNTYPTTF GOTTYEILL TVAAPSVFLF PPSEDEQLKSG TASVCLNN FYPREAKVW KVDNALQSGN SQBSVTEQDS KOSTYSLST  
LTLSKADYEK HKVYACEVTH QGLSSPVTKS FNRGEC  
LTLSKADYEK HKVYACEVTH QGLSSPVTKS FNRGEC

FIG. 19E